

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.3953 Seconds
(without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613B-2

Perfect score: 578
Sequence: 1 QDWLTFQKKHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:virus:*
16: SP:bacteriaph:*
17: SP:archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	127	13	Q918V8 rana pipien
2	556	96.2	127	13	Q8UVX5 rana pipien
3	404.5	70.0	129	13	Q9DXY6 rana catesb
4	386	66.8	128	13	Q9DXY8 rana catesb
5	311	53.8	128	13	Q9DXY7 rana catesb
6	309	53.5	128	13	Q9DXY5 rana catesb
7	298	51.6	133	13	Q98SM0 rana catesb
8	292	50.5	133	13	Q9PWR7 rana catesb
9	286	49.5	133	13	Q98SL9 rana catesb
10	285	49.3	132	13	Q98SM2 rana catesb
11	282	48.8	133	13	Q98SL8 rana catesb
12	280	48.4	132	13	Q98SM1 rana catesb
13	275.5	47.7	132	13	Q9DF78 rana catesb
14	157.5	27.2	169	13	Q9W738 xenopus lae
15	129	22.3	152	11	Q9JKT5 mus saxicol
16	127	22.0	157	11	Q9JKT9 meriones un

17	126.5	21.9	153	11	Q9JKT7	Q9JKT7 mus saxicol
18	126	21.8	157	11	Q9JKT3	Q9JKT3 meriones un
19	125	21.6	157	11	Q9JKT4	Q9JKT4 meriones un
20	123	21.3	154	11	Q9JKT8	Q9JKT8 mus saxicol
21	122	21.1	157	11	Q9JKT1	Q9JKT1 meriones un
22	121	20.9	157	11	Q9JKT2	Q9JKT2 meriones un
23	120.5	20.8	155	11	Q9JKT9	Q9JKT9 mus pahari
24	119.5	20.7	155	11	Q9JKT3	Q9JKT3 mus saxicol
25	116.5	20.2	155	11	Q9JKT6	Q9JKT6 mus saxicol
26	115.5	20.0	132	6	Q9TV25	Q9TV25 eulemur ful
27	115.5	20.0	155	11	Q9JKT4	Q9JKT4 mus saxicol
28	115.5	20.0	155	11	Q9JKT2	Q9JKT2 mus saxicol
29	114.5	19.8	170	6	Q9BEC1	Q9BEC1 treagus ja
30	113.5	19.6	119	6	Q9TS06	Q9TS06 cercopithec
31	113.5	19.6	119	6	Q9TV30	Q9TV30 gorilla gor
32	113.5	19.6	132	6	Q9TV24	Q9TV24 galago moho
33	113.5	19.6	155	11	Q9R134	Q9R134 ratius notv
34	113	19.6	156	11	Q9JKT7	Q9JKT7 mus caroli
35	113	19.6	156	11	Q9JKT6	Q9JKT6 mus caroli
36	112.5	19.5	119	6	Q9TV30	Q9TV30 saquinus oe
37	112.5	19.5	155	11	Q9R125	Q9R125 mus musculi
38	112.5	19.5	155	11	Q9JKT8	Q9JKT8 mus pahari
39	112	19.4	124	6	Q9TSP2	Q9TSP2 bos taurus
40	112	19.4	156	11	Q9JKT7	Q9JKT7 mus caroli
41	111.5	19.3	155	11	Q9JKT3	Q9JKT3 mus caroli
42	111	19.2	124	6	Q9SNE6	Q9SNE6 bubalus bub
43	111	19.2	156	6	Q8S004	Q8S004 lemur catia
44	111	19.2	156	11	Q9JKT5	Q9JKT5 mus caroli
45	111	19.2	156	11	Q9JKT4	Q9JKT4 mus caroli

ALIGNMENTS

RESULT 1

ID	Q918V8	PRELIMINARY:	PRT:	127 AA.
AC	Q918V8;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Onconase variant rapLRI precursor.			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=20330357; PubMed=10871370;			
RA	Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;			
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a			
RT	3' UTR of unusual length and structure."			
RL	Nucleic Acids Res. 28:2375-2382(2000).			
DR	EMBL: AF165133; AAF76935.1;			
DR	HSSP: P22069; IONC.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA.1.			
DR	ProDom: PD000535; RNaseA.1.			
DR	SMART: SM00092; RNase_PC.1.			
DR	PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL			
FT	1 23 POTENTIAL.			
SQ	SEQUENCE 127 AA; 14491 MW; B851IDC5407AB69B CRC64;			

Query Match 100.0%; Score 578; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 3e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLNTRDVCNINIMSTNLFHCKDKNTFTYSRPEYKAKCKIISKVLT 60
DB 24 QDWLTFQKKHLNTRDVCNINIMSTNLFHCKDKNTFTYSRPEYKAKCKIISKVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 127

RESULT 2

ID Q8UVX5 PRELIMINARY: PRT: 127 AA.
 AC Q8UVX5;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Onconase precursor.
 GN RPR.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liao Y.-D., Wang S.-C.;
 RT "Rana pipiens onconase genomic DNA";
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF332139; AAL54383.1;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 23 POTENTIAL.
 SQ SEQUENCE 127 AA: 14469 MW: 953F90D351CFEEF3 CRC64;
 Query Match
 Best Local Similarity 96.2%; Score 556; DB 13; Length 127;
 Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAKGIIASKNVLT 60
 DB 24 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAKGIIASKNVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 127

RESULT 3
 ID Q9DFY6 PRELIMINARY: PRT: 129 AA.
 AC Q9DFY6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNaseA ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Liver.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tissue=Liver.
 RL Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 DR Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF242555; AAG31441.2;
 DR HSP: P22069; IONC.

DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 23 POTENTIAL.
 SQ SEQUENCE 129 AA: 14724 MW: 826A62882B10ABDA CRC64;

Query Match
 Best Local Similarity 70.0%; Score 404.5; DB 13; Length 129;
 Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 1 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAKGIIASKNVLT 60
 DB 24 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAKGIIASKNVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 128

RESULT 4

ID Q9DFY8 PRELIMINARY: PRT: 128 AA.
 AC Q9DFY8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNaseA ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Liver.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tissue=Liver.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 DR Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF242555; AAG31439.1;
 DR HSP: P22069; IONC.

DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA.1.
 DR ProDom: PD000535; RNaseA.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 23 POTENTIAL.
 SQ SEQUENCE 128 AA: 14839 MW: 989719CF52053ECC CRC64;

Query Match
 Best Local Similarity 66.8%; Score 386; DB 13; Length 128;
 Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

OY 1 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAKGIIASKNVLT 60
 DB 24 QDWLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFYSRPEPKAKGIIASKNVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 104
 DB 84 SEFYLSDCNVTSRPCKYKLTSTNTEFCVTCENQAPVHFVGHC 127

RESULT	9
C98SL9	
ID	C98SL9
AC	PRELIMINARY;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	RNase A-type ribonuclease rc212 precursor.
OS	Rana catesbeiana (Bull frog).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX	NCBI_TaxID=8400;
RP	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21539506; PubMed=11683320;
RT	Rosenberg H.F., Zhang J., Llae Y.-D., Dyer K.D.;
RT	"Rapid diversification of RNase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana.";
RL	J. Mol. Evol. 53:31-38(2001);
DR	EMBL; AF351210; AAAK30256.1; -
DR	HSSP; P11916; BC4.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; rnaseaA.1.
DR	prodom; PD000535; RNaseA; 1.
DR	SMART; SM00092; RNase_Fc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL
SEQ	SEQUENCE 133 AA; 14615 MW; C6785B236B2E54E CRC64;
	POTENTIAL.
Query Match	49.5%; Score 286; DB 13; Length 133;
Best Local Similarity	47.7%; Pred. NO. 6e-25;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;	

[illegible]

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RX MEDLINE-21539506; PubMed-11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rana A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
J. Mol. Evol. 53:31-38(2001)
DR EMBL: AF351211; AAK30257.1;
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
Query Match 48.8%; Score 282; DB 13; Length 133;
Best Local Similarity 46.8%; Pred. No. 1.7e-24;
Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFQKHLNTRDVCNNINSTNLF---HCKDKNTFYSPREPVKATCKGIASKN 56
DB 23 QNATFPOQHITNTSSINCNSIMNNSLYIGGCKKNTFIASATTVKIGICSG-VTDK 81
QY 57 VLTSEFYISDCN--VTSRPCKYKLRKSTNTPFCVTCENQAPVHFGVGHG 104
DB 82 VLSTTRFOLKXXYTRTFITSRPCPSYSTRKTKICVCKENEPVHFGIGKC 132

RESULT 12
Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21539506; PubMed-11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rana A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
J. Mol. Evol. 53:31-38(2001)
DR EMBL: AF351208; AAK30254.1;
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
Query Match 48.4%; Score 280; DB 13; Length 132;
Best Local Similarity 46.8%; Pred. No. 2.9e-24;
Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

QY 1 QDWLTFQKHLNTRDVCNNINSTNLF---HCKDKNTFYSPREPVKATCKGIASKN 56
DB 23 QNATFPOQHITNTSSINCNSIMNNSLYIGGCKKNTFIASATTVKIGICTVLSN-N 81
QY 57 VLTSEFYISDCN--VTSRPCKYKLRKSTNTPFCVTCENQAPVHFGVGHG 104
DB 82 VLSTTRFOLKXXYTRTFITSRPCPSYSTRKTKICVCKENEPVHFGIGKC 132

RESULT 13

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Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNaseII ribonuclease precursor.
DE Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE-20512555; PubMed-11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF288642; AAG30414.2;
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 2 132 RC-RNASEII RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;
Query Match 47.7%; Score 275.5; DB 13; Length 132;
Best Local Similarity 44.1%; Pred. No. 9.4e-24;
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

QY 1 QDWLTFQKHLNTRDVCNNINSTNLF---HCKDKNTFYSPREPVKATCKGIASKN 56
DB 22 QNMAKFKERKLTSTSSIDCNTIMDKAIYIGGCKKERNTFISSSEDNVKAICSCVSPDRK 81
QY 57 VLTSEFYISDCN--NVTSRPCKYKLRKSTNTPFCVTCENQAPVHFGVGHG 104
DB 82 ELSTTSFKLNTCTIDSTITPRCPYHPSPDNNKICVCKEKQLPVHFGIGKC 132

RESULT 14
Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96069863; PubMed-7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the fGF receptor by a
RT yeast screening method and their activity in Xenopus development."
Cell 83:621-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;

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